



results of BLAST

BLASTN 2.2.9 [May-01-2004]

RID: 1091213456-3749-21682658804.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
2,314,858 sequences; 11,275,552,939 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

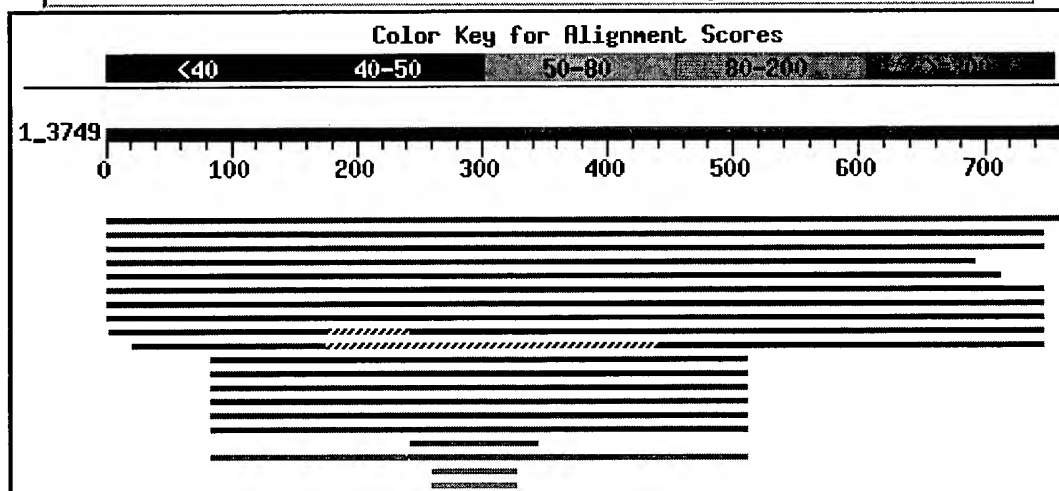
[Taxonomy reports](#)

Query=

(759 letters)

Distribution of 40 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 37182172 gb AY358525.1 	Homo sapiens clone DNA66519 GRVS...	1460	0.0	U
gi 34101277 ref NM_183065.1 	Homo sapiens hypothetical prot...	1436	0.0	LU
gi 34101275 ref NM_032354.2 	Homo sapiens hypothetical prot...	1358	0.0	LU
gi 13751659 gb AF311338.1 AF311338	Homo sapiens DC20 mRNA, ...	1219	0.0	LU G
gi 47123436 gb BC070231.1 	Homo sapiens cDNA clone MGC:8821...	1160	0.0	U
gi 14042769 dbj AK027813.1 	Homo sapiens cDNA FLJ14907 fis,...	660	0.0	LG
gi 24421745 gb AC129492.6 	Homo sapiens chromosome 17, clon...	592	e-166	

gi 27764773 gb AC106019.4 	Homo sapiens chromosome 17, clon...	592	e-166	
gi 34534999 dbj AK127891.1 	Homo sapiens cDNA FLJ45997 fis,...	592	e-166	U
gi 33871186 gb BC006292.2 	Homo sapiens hypothetical protei...	590	e-165	LUG
gi 12834052 dbj AK003403.1 	Mus musculus 18-day embryo whol...	523	e-145	LUG
gi 12833055 dbj AK002804.1 	Mus musculus adult male kidney ...	523	e-145	LUG
gi 21539608 ref NM_025838.1 	Mus musculus RIKEN cDNA 111000...	523	e-145	LU
gi 34870918 ref XM_213332.2 	Rattus norvegicus similar to R...	512	e-142	LU
gi 12850001 dbj AK012938.1 	Mus musculus 10, 11 days embryo...	433	e-118	LUG
gi 21539634 ref NM_028336.1 	Mus musculus RIKEN cDNA 111000...	433	e-118	LUG
gi 1028384 emb Z57153.1 HS165G2F	H.sapiens CpG island DNA g...	191	3e-45	
gi 20068638 emb AL645902.6 	Mouse DNA sequence from clone R...	154	3e-34	
gi 41351479 gb BC065897.1 	Danio rerio zgc:77926, mRNA (cDN...	56	8e-05	LU
gi 47086012 ref NM_213211.1 	Danio rerio zgc:77926 (zgc:779...	56	8e-05	LU

Alignments

Get selected sequences

Select all

Deselect all

☐ [>gi|37182172|gb|AY358525.1|](#) **U** Homo sapiens clone DNA66519 GRVS638 (UNQ638) mRNA,
Length = 759

Score = 1460 bits (759), Expect = 0.0

Identities = 747/759 (98%)

Strand = Plus / Plus

```

Query: 1   ctagatttgtcggcttgcgaggagacttcaggagtcgctgtctctgaacttcagcctca 60
          |||
Sbjct: 1   ctagatttgtcggcttgcgaggagacttcaggagtcgctgtctctgaacttcagcctca 60

Query: 61   gagaccgccgacctgtccccgagggccatgggcccgggtctcagggttggtgcctctcg 120
          |||
Sbjct: 61   gagaccgccgacctgtccccgagggccatgggcccgggtctcagggttggtgcctctcg 120

Query: 121  cttcctgacgctcctggcgcatctgggtggcgatcaccttattctgggtcccgggacag 180
          |||
Sbjct: 121  cttcctgacgctcctggcgcatctgggtggcgatcaccttattctgggtcccgggacag 180

Query: 181  caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 240
          |||
Sbjct: 181  caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 240

Query: 241  tcagctgggtggccgcgctctctgtcacccctgggcctctttgcagtggagctggccggttt 300
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Sbjct: 241  tcagctgggtggccgcgctctctgtcacccctgggcctctttgcagtggagctggccggttt 300

Query: 301  cctctcaggagtctccatgttcaacagcacccagagcctcatctccattggggctcactg 360
          |||

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Sbjct: 301 cctctcaggagctctccatgttcaacagcaccagagcctcatctccattggggctcactg 360

Query: 361 tagtgcacccgtggccctgtccttcttcatattcgagcgttgggagtgactacgtattg 420
|||||

Sbjct: 361 tagtgcacccgtggccctgtccttcttcatattcgagcgttgggagtgactacgtattg 420

Query: 421 gtacatTTTTgtcttctgcagtgcccttccagctgtcactgaaatggctttattcgtcac 480
|||||

Sbjct: 421 gtacatTTTTgtcttctgcagtgcccttccagctgtcactgaaatggctttattcgtcac 480

Query: 481 cgtctttgggctgaaaaagaaacccttctgattaccttcatgacgggaacctaaggacga 540
|||||

Sbjct: 481 cgtctttgggctgaaaaagaaacccttctgattaccttcatgacgggaacctaaggacga 540

Query: 541 agcctacaggggcaagggccgcttcgtattcctggaagaaggaaggcataggcttcggtt 600
|||||

Sbjct: 541 agcctacaggggcaagggccgcttcgtattcctggaagaaggaaggcataggcttcggtt 600

Query: 601 ttccccctcggaactgcttctgctggaggatatgtgttgaataattacgtcttgagtct 660
|||||

Sbjct: 601 ttccccctcggaactgcttctgctggaggatatgtgttgaataattacgtcttgagtct 660

Query: 661 gggattatccgcattgtatttagtgctttgtaataaaatatgtttttagtaacattaag 720
|||||

Sbjct: 661 gggattatccgcattgtatttagtgctttgtaataaaatatgtttttagtaacattaag 720

Query: 721 acttatatacagttttaggggacaattnnnnnnnnnnnn 759
|||||

Sbjct: 721 acttatatacagttttaggggacaattaaaaaaaaaaaa 759

☐ >gi|34101277|ref|NM_183065.1| **LU** Homo sapiens hypothetical protein MGC10744 (MG
variant 2, mRNA
Length = 1507

Score = 1436 bits (747), Expect = 0.0

Identities = 747/747 (100%)

Strand = Plus / Plus

Query: 1 ctagatttgtcggttgccgggagacttcaggagtcgctgtctctgaacttccagcctca 60
|||||

Sbjct: 18 ctagatttgtcggttgccgggagacttcaggagtcgctgtctctgaacttccagcctca 77

Query: 61 gagaccgcgcgccttgtccccgagggccatgggccgggtctcagggttgtgccctctcg 120
|||||

Sbjct: 78 gagaccgcgcgccttgtccccgagggccatgggccgggtctcagggttgtgccctctcg 137

Query: 121 cttcctgacgctcctggcgcatctggtggtcgatcaccttattctggtcccgggacag 180
|||||

Sbjct: 138 cttcctgacgctcctggcgcatctggtggctcgatcaccttattctgggtcccgaggacag 197

Query: 181 caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 240
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Sbjct: 198 caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 257

Query: 241 tcagctggtggccgctctctgtcacccctgggcctctttgcagtggagctggccggttt 300
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Sbjct: 258 tcagctggtggccgctctctgtcacccctgggcctctttgcagtggagctggccggttt 317

Query: 301 cctctcaggagtctccatgttcaacagcacccagagcctcatctccattggggctcactg 360
 |||

Sbjct: 318 cctctcaggagtctccatgttcaacagcacccagagcctcatctccattggggctcactg 377

Query: 361 tagtgcacccgtggccctgtccttcttcatattcgagcgttgggagtgcactacgtattg 420
 |||

Sbjct: 378 tagtgcacccgtggccctgtccttcttcatattcgagcgttgggagtgcactacgtattg 437

Query: 421 gtacatTTTTgtcttctgcagtgcccttccagctgtcactgaaatggctttattcgtcac 480
 |||

Sbjct: 438 gtacatTTTTgtcttctgcagtgcccttccagctgtcactgaaatggctttattcgtcac 497

Query: 481 cgtctttgggctgaaaaagaaacccttctgattaccttcatgacgggaacctaaggacga 540
 |||

Sbjct: 498 cgtctttgggctgaaaaagaaacccttctgattaccttcatgacgggaacctaaggacga 557

Query: 541 agcctacaggggcaagggccgcttcgtattcctggaagaaggaaggcataggcttcggtt 600
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Sbjct: 558 agcctacaggggcaagggccgcttcgtattcctggaagaaggaaggcataggcttcggtt 617

Query: 601 ttcccctcgaaactgcttctgctggaggatatgtgttggaataattacgtcttgagtct 660
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Sbjct: 618 ttcccctcgaaactgcttctgctggaggatatgtgttggaataattacgtcttgagtct 677

Query: 661 gggattatccgcattgtatttagtgctttgtaataaaatatgtttttagtaacattaag 720
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Sbjct: 678 gggattatccgcattgtatttagtgctttgtaataaaatatgtttttagtaacattaag 737

Query: 721 acttatatacagtttttaggggacaatt 747
 |||

Sbjct: 738 acttatatacagtttttaggggacaatt 764

☐ >gi|34101275|ref|NM_032354.2| **LU** Homo sapiens hypothetical protein MGC10744 (MG
 variant 1, mRNA
 Length = 1533

Score = 1358 bits (706), Expect = 0.0
 Identities = 747/765 (97%), Gaps = 18/765 (2%)

Strand = Plus / Plus

Query: 1 ctagatttgtcggcttgcgaggagacttcaggagtcgctgtctctgaacttccagcctca 60
|||||
Sbjct: 26 ctagatttgtcggcttgcgaggagacttcaggagtcgctgtctctgaacttccagcctca 85

Query: 61 gagaccgccccttggtccccgagggccatgggcccgggtctcagggcttggtgccctctcg 120
|||||
Sbjct: 86 gagaccgccccttggtccccgagggccatgggcccgggtctcagggcttggtgccctctcg 145

Query: 121 cttcctgacgctcctggcgcatctggtggctcgtcatcaccttattctggtcccgggacag 180
|||||
Sbjct: 146 cttcctgacgctcctggcgcatctggtggctcgtcatcaccttattctggtcccgggacag 205

Query: 181 caacatacaggcctgctgctctcacgttcacccccgaggagtatgacaagcaggacat 240
|||||
Sbjct: 206 caacatacaggcctgctgctctcacgttcacccccgaggagtatgacaagcaggacat 265

Query: 241 tca-----gctgggtggccgcgctctctgtcaccctgggcctctttgc 282
||| |||||
Sbjct: 266 tcatccacttcctctctgcaggctggtggccgcgctctctgtcaccctgggcctctttgc 325

Query: 283 agtggagctggccggtttcctctcaggagttccatgttcaacagcaccagagcctcat 342
|||||
Sbjct: 326 agtggagctggccggtttcctctcaggagttccatgttcaacagcaccagagcctcat 385

Query: 343 ctccattggggctcactgtagtgcacccgtggccctgtccttcttcatttcgagcgttg 402
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Sbjct: 386 ctccattggggctcactgtagtgcacccgtggccctgtccttcttcatttcgagcgttg 445

Query: 403 ggagtgcactacgtattggtacatttttgtcttctgcagtgccttccagctgtcactga 462
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Sbjct: 446 ggagtgcactacgtattggtacatttttgtcttctgcagtgccttccagctgtcactga 505

Query: 463 aatggctttattcgtcaccgtctttgggctgaaaaagaaacccttctgattaccttcag 522
|||||
Sbjct: 506 aatggctttattcgtcaccgtctttgggctgaaaaagaaacccttctgattaccttcag 565

Query: 523 acgggaacctaaaggacgaagcctacaggggcaagggccgcttcgtattcctggaagaagg 582
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Sbjct: 566 acgggaacctaaaggacgaagcctacaggggcaagggccgcttcgtattcctggaagaagg 625

Query: 583 aaggcataggcttcggttttccctcggaactgcttctgctggaggatatgtgttgaa 642
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Sbjct: 626 aaggcataggcttcggttttccctcggaactgcttctgctggaggatatgtgttgaa 685

Query: 643 taattacgtcttgagtctgggattatccgcattgtatttagtgctttgtaataaaatatg 702
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Sbjct: 686 taattacgtcttgagtcctgggattatccgcattgtatttagtgctttgtaataaaatatg 745

Query: 703 tttttagtaacattaagacttatatacagtttttaggggacaatt 747

|||||

Sbjct: 746 tttttagtaacattaagacttatatacagtttttaggggacaatt 790

☐ >gi|13751659|gb|AF311338.1|AF311338 **LUG** Homo sapiens DC20 mRNA, complete cds
Length = 826

Score = 1219 bits (634), Expect = 0.0

Identities = 691/712 (97%), Gaps = 20/712 (2%)

Strand = Plus / Plus

Query: 1 ctagatttgctcggttcgctgggagacttcaggagtcgctgtctctgaacttcagcctca 60

|||||

Sbjct: 77 ctagatttgctcggttcgctgggagacttcaggagtcgctgtctctgaacttcagcctca 136

Query: 61 gagaccgccgaccttgctcccgagggccatgggcccgggtctcagggttggtgccctctcg 120

|||||

Sbjct: 137 gagaccgccgaccttgctcccgagggccatgggcccgggtctcagggttggtgccctctcg 196

Query: 121 cttcctgacgctcctggcgcatctggtggcgtcatcaccttattctggtcccgggacag 180

|||||

Sbjct: 197 cttcctgacgctcctggcgcatctggtggcgtcatcaccttattctggtcccgggacag 256

Query: 181 caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 240

|||||

Sbjct: 257 caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 316

Query: 241 tca-----gctggtggccgcgctctctgtcacctggg-cctctttg 281

||| |||||

Sbjct: 317 tcatccaacttcctctctgcagggtggtggccgcgctctctgtcacctggggcctctttg 376

Query: 282 cagtggagctggccggtttcctctcaggagtctccatgttcaacagcaccc-agagcctc 340

|||||

Sbjct: 377 cagtggagctggccggtttcctctcaggagtctccatgttcaacagcacccagagcctc 436

Query: 341 atctccattggggctcactgtagtgcatccgtggccctgtccttcttcatattcgagcgt 400

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Sbjct: 437 atctccattggggctcactgtagtgcatccgtggccctgtccttcttcatattcgagcgt 496

Query: 401 tgggagtgactacgtattggtacatttttgtcttctgcagtgcccttcagctgtcact 460

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Sbjct: 497 tgggagtgactacgtattggtacatttttgtcttctgcagtgcccttcagctgtcact 556

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

|||||

Sbjct: 557 gaaatggctttattcgtcacctgtcttgggctgaaaaagaaacccttctgattaccttca 616

Query: 521 tgacgggaacctaaggacgaagcctacaggggcaagggccgcttcgtattcctggaagaa 580
|||||
Sbjct: 617 tgacgggaacctaaggacgaagcctacaggggcaagggccgcttcgtattcctggaagaa 676

Query: 581 ggaaggcataggcttcggttttccctcggaactgcttctgctggaggatatgtgttg 640
|||||
Sbjct: 677 ggaaggcataggcttcggttttccctcggaactgcttctgctggaggatatgtgttg 736

Query: 641 aataattacgtcttgagctctgggattatccgcattgtatttagtgctttgta 692
|||||
Sbjct: 737 aataattacgtcttgagctctgggattatccgcattgtatttagtgctttgta 788

 >gi|47123436|gb|BC070231.1|  Homo sapiens cDNA clone MGC:88213 IMAGE:6617879, c
Length = 754

Score = 1160 bits (603), Expect = 0.0
Identities = 691/730 (94%), Gaps = 39/730 (5%)
Strand = Plus / Plus

Query: 1 ctagatttgtcggcttgcggggagacttcaggagtcgctgtctctgaactccagcctca 60
|||||
Sbjct: 15 ctagatttgtcggcttgcggggagacttcaggagtcgctgtctctgaactccagcctca 74

Query: 61 gagaccgccgcccttggtcccgagggccatgggccgggtctcagggcttggtccctctcg 120
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Sbjct: 75 gagaccgccgcccttggtcccgagggccatgggccgggtctcagggcttggtccctctcg 134

Query: 121 cttcctgacgctcctggcgcatctggtggtcgatcaccttattctggtcccgggacag 180
|||||
Sbjct: 135 cttcctgacgctcctggcgcatctggtggtcgatcaccttattctggtcccgggacag 194

Query: 181 caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 240
|||||
Sbjct: 195 caacatacaggcctgcctgcctctcacgttcacccccgaggagtatgacaagcaggacat 254

Query: 241 tca-----gctggtggccgcgctctctgtcaccctgggcctctttgc 282
||| |||||
Sbjct: 255 tcatccacttctctctgcaggctggtggccgcgctctctgtcaccctgggcctctttgc 314

Query: 283 agtggagctggccggtttcctctcaggagctctccatgttcaacagcaccagagcctcat 342
|||||
Sbjct: 315 agtggagctggccggtttcctctcaggagctctccatgttcaacagcaccagagcctcat 374

Query: 343 ctccattggggctcactgtagtgcatccgtggccctgtccttcttcatattcgagcgttg 402
|||||
Sbjct: 375 ctccattggggctcactgtagtgcatccgtggccctgtccttcttcatattcgagcgttg 434

Query: 242 cagctggtggccgcgctctctgtcaccctgggcctctttgcagtggagctggccggtttc 301
|||||
Sbjct: 241 cagctggtggccgcgctctctgtcaccctgggcctctttgcagtggagctggccggtttc 300

Query: 302 ctctcaggagtctccatgttcaacagcaccagagcctcatct 344
|||||
Sbjct: 301 ctctcaggagtctccatgttcaacagcaccagagcctcatct 343

Score = 592 bits (308), Expect = e-166
Identities = 308/308 (100%)
Strand = Plus / Plus

Query: 440 agtgcccttccagctgtcactgaaatggctttattcgtcaccgtctttgggctgaaaaag 499
|||||
Sbjct: 1826 agtgcccttccagctgtcactgaaatggctttattcgtcaccgtctttgggctgaaaaag 1885

Query: 500 aaacccttctgattaccttcatgacgggaacctaaggacgaagcctacaggggcaagggc 559
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Sbjct: 1886 aaacccttctgattaccttcatgacgggaacctaaggacgaagcctacaggggcaagggc 1945

Query: 560 cgcttcgtattcctggaagaaggaaggcataggcttcggttttcccctcggaactgctt 619
|||||
Sbjct: 1946 cgcttcgtattcctggaagaaggaaggcataggcttcggttttcccctcggaactgctt 2005

Query: 620 ctgctggaggatatgtggttgaataattacgtcttgagtctgggattatccgcattgtat 679
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Sbjct: 2006 ctgctggaggatatgtggttgaataattacgtcttgagtctgggattatccgcattgtat 2065

Query: 680 ttagtgctttgtaataaaatatgtttttagtaacattaagacttatatacagttttagg 739
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Sbjct: 2066 ttagtgctttgtaataaaatatgtttttagtaacattaagacttatatacagttttagg 2125

Query: 740 ggacaatt 747
|||||
Sbjct: 2126 ggacaatt 2133

Score = 187 bits (97), Expect = 4e-44
Identities = 97/97 (100%)
Strand = Plus / Plus

Query: 345 ccattggggctcactgtagtgcacccgtggccctgtccttcttcatttcgagcggttggg 404
|||||
Sbjct: 1484 ccattggggctcactgtagtgcacccgtggccctgtccttcttcatttcgagcggttggg 1543

Query: 405 agtgcactacgtatttggtacatttttgtcttctgcag 441
|||||
Sbjct: 1544 agtgcactacgtatttggtacatttttgtcttctgcag 1580

☐ >gi|24421745|gb|AC129492.6| ☒ Homo sapiens chromosome 17, clone RP11-599B13, com
Length = 196037

Score = 592 bits (308), Expect = e-166
Identities = 308/308 (100%)
Strand = Plus / Minus

Query: 440 agtgcccttcagctgtcactgaaatggctttattcgtcacctgtctttgggctgaaaaag 499
|||||
Sbjct: 169150 agtgcccttcagctgtcactgaaatggctttattcgtcacctgtctttgggctgaaaaag 169091

Query: 500 aaacccttctgattaccttcatgacgggaacctaaggacgaagcctacaggggcaagggc 559
|||||
Sbjct: 169090 aaacccttctgattaccttcatgacgggaacctaaggacgaagcctacaggggcaagggc 169031

Query: 560 cgcttcgtattcctggaagaaggaaggcataggcttcggttttccctcgaaactgctt 619
|||||
Sbjct: 169030 cgcttcgtattcctggaagaaggaaggcataggcttcggttttccctcgaaactgctt 168971

Query: 620 ctgctggaggatatgtgttgaataattacgtcttgagtctgggattatccgcattgtat 679
|||||
Sbjct: 168970 ctgctggaggatatgtgttgaataattacgtcttgagtctgggattatccgcattgtat 168911

Query: 680 ttagtgctttgtaataaaaatatgtttttagtaacattaagacttatatacagttttagg 739
|||||
Sbjct: 168910 ttagtgctttgtaataaaaatatgtttttagtaacattaagacttatatacagttttagg 168851

Query: 740 ggacaatt 747
|||||
Sbjct: 168850 ggacaatt 168843

Score = 339 bits (176), Expect = 7e-90
Identities = 176/176 (100%)
Strand = Plus / Minus

Query: 1 ctagatttgtcggttgcggggagacttcaggagtcgctgtctctgaacttccagcctca 60
|||||
Sbjct: 171250 ctagatttgtcggttgcggggagacttcaggagtcgctgtctctgaacttccagcctca 171191

Query: 61 gagaccgcccgttgtccccgagggccatgggcccgggtctcagggcttgtgccctctcg 120
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Sbjct: 171190 gagaccgcccgttgtccccgagggccatgggcccgggtctcagggcttgtgccctctcg 171131

Query: 121 cttcctgacgctcctggcgcatctggtggtcgatcaccttattctggtcccggg 176
|||||
Sbjct: 171130 cttcctgacgctcctggcgcatctggtggtcgatcaccttattctggtcccggg 171075